

	Pro Leu Phe Gly Ala Gly Ser Ile Ser Ser Gly Glu Leu Tyr Ile Asp			
	595	600	605	
5	Lys Ile Glu Ile Ile Leu Ala Asp Ala Thr Phe Glu Ala Glu Ser Asp			
	610	615	620	
	Leu Glu Arg Ala Gln Lys Ala Val Asn Ala Leu Phe Thr Ser Ser Asn			
	625	630	635	640
10	Gln Ile Gly Leu Lys Thr Asp Val Thr Asp Tyr His Ile Asp Gln Val			
	645	650	655	
15	Ser Asn Leu Val Asp Cys Leu Ser Asp Glu Phe Cys Leu Asp Glu Lys			
	660	665	670	
	Arg Glu Leu Ser Glu Lys Val Lys His Ala Lys Arg Leu Ser Asp Glu			
	675	680	685	
20	Arg Asn Leu Leu Gln Asp Pro Asn Phe Arg Gly Ile Asn Arg Gln Pro			
	690	695	700	
	Asp Arg Gly Trp Arg Gly Ser Thr Asp Ile Thr Ile Gln Gly Gly Asp			
	705	710	715	720
25	Asp Val Phe Lys Glu Asn Tyr Val Thr Leu Pro Gly Thr Val Asp Glu			
	725	730	735	
	Cys Tyr Pro Thr Tyr Leu Tyr Gln Lys Ile Asp Glu Ser Lys Leu Lys			
30	740	745	750	
	Ala Tyr Thr Arg Tyr Glu Leu Arg Gly Tyr Ile Glu Asp Ser Gln Asp			
	755	760	765	
35	Leu Glu Ile Tyr Leu Ile Arg Tyr Asn Ala Lys His Glu Ile Val Asn			
	770	775	780	
	Val Pro Gly Thr Gly Ser Leu Trp Pro Leu Ser Ala Gln Ser Pro Ile			
	785	790	795	800
40	Gly Lys Cys Gly Glu Pro Asn Arg Cys Ala Pro His Leu Glu Trp Asn			
	805	810	815	
	Pro Asp Leu Asp Cys Ser Cys Arg Asp Gly Glu Lys Cys Ala His His			
45	820	825	830	
	Ser His His Phe Thr Leu Asp Ile Asp Val Gly Cys Thr Asp Leu Asn			
	835	840	845	
50	Glu Asp Leu Gly Val Trp Val Ile Phe Lys Ile Lys Thr Gln Asp Gly			
	850	855	860	
	His Ala Arg Leu Gly Asn Leu Glu Phe Leu Glu Lys Pro Leu Leu			
	865	870	875	880

	Gly Glu Ala Leu Ala Arg Val Lys Arg Ala Glu Lys Lys Trp Arg Asp		
	885	890	895
5	Lys Arg Glu Lys Leu Gln Leu Glu Thr Asn Ile Val Tyr Lys Glu Ala		
	900	905	910
	Lys Glu Ser Val Asp Ala Leu Phe Val Asn Ser Gln Tyr Asp Arg Leu		
10	915	920	925
	Gln Val Asp Thr Asn Ile Ala Met Ile His Ala Ala Asp Lys Arg Val		
	930	935	940
15	His Arg Ile Arg Glu Ala Tyr Leu Pro Glu Leu Ser Val Ile Pro Gly		
	945	950	955
	960		
	Val Asn Ala Ala Ile Phe Glu Glu Leu Glu Gly Arg Ile Phe Thr Ala		
	965	970	975
20	Tyr Ser Leu Tyr Asp Ala Arg Asn Val Ile Lys Asn Gly Asp Phe Asn		
	980	985	990
	Asn Gly Leu Leu Cys Trp Asn Val Lys Gly His Val Asp Val Glu Glu		
25	995	1000	1005
	Gln Asn Asn His Arg Ser Val Leu Val Ile Pro Glu Trp Glu Ala Glu		
	1010	1015	1020
30	Val Ser Gln Glu Val Arg Val Cys Pro Gly Arg Gly Tyr Ile Leu Arg		
	1025	1030	1035
	1040		
	Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His		
35	1045	1050	1055
	Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu		
	1060	1065	1070
	Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly		
40	1075	1080	1085
	Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr		
	1090	1095	1100
	Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser		
45	1105	1110	1115
	1120		
	Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys		
	1125	1130	1135
50	Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr		
	1140	1145	1150
	Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile		
	1155	1160	1165

Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
1170 1175 1180

5 Leu Leu Met Glu Glu
1185

10 (2) INFORMATION FOR SEQ ID NO:7:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3567 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..3567

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GAG GAA AAT AAT CAA AAT CAA TGC ATA CCT TAC AAT TGT TTA AGT Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser	48
1 5 10 15	
AAT CCT GAA GAA GTA CTT TTG GAT GGA GAA CGG ATA TCA ACT GGT AAT Asn Pro Glu Glu Val Leu Leu Asp Gly Glu Arg Ile Ser Thr Gly Asn	96
20 25 30	
TCA TCA ATT GAT ATT TCT CTG TCA CTT GTT CAG TTT CTG GTA TCT AAC Ser Ser Ile Asp Ile Ser Leu Ser Leu Val Gln Phe Leu Val Ser Asn	144
35 40 45	
TTT GTA CCA GGG GGA GGA TTT TTA GTT GGA TTA ATA GAT TTT GTA TGG Phe Val Pro Gly Gly Phe Leu Val Gly Leu Ile Asp Phe Val Trp	192
50 55 60	
GGA ATA GTT GGC CCT TCT CAA TGG GAT GCA TTT CTA GTA CAA ATT GAA Gly Ile Val Gly Pro Ser Gln Trp Asp Ala Phe Leu Val Gln Ile Glu	240
65 70 75 80	
CAA TTA ATT AAT GAA AGA ATA GCT GAA TTT GCT AGG AAT GCT GCT ATT Gln Leu Ile Asn Glu Arg Ile Ala Glu Phe Ala Arg Asn Ala Ala Ile	288
85 90 95	
GCT AAT TTA GAA GGA TTA GGA AAC AAT TTC AAT ATA TAT GTG GAA GCA Ala Asn Leu Glu Gly Leu Gly Asn Asn Phe Asn Ile Tyr Val Glu Ala	336
100 105 110	
50 TTT AAA GAA TGG GAA GAT GAT CCT CAT AAT CCC ACA ACC AGG ACC AGA Phe Lys Glu Trp Glu Asp Asp Pro His Asn Pro Thr Thr Arg Thr Arg	384
115 120 125	